

What is claimed is:

1. A genetically modified plant comprising at least one exogenous antisense FT-encoding nucleotide sequence in its genome and having the phenotype of delayed flower development.

2. The genetically modified plant of claim 1, wherein the antisense exogenous FT-encoding nucleotide sequence has at least 80% sequence homology to SEQ ID NO:3

3. The genetically modified plant of claim 1, wherein the antisense exogenous FT-encoding nucleotide sequence has at least 85% homology to SEQ ID NOS:3.

4. The genetically modified plant of claim 1, wherein the antisense exogenous FT-encoding nucleotide sequence has at least 90% homology to SEQ ID NOS:3.

5. The genetically modified plant of claim 1, wherein the antisense exogenous FT-encoding nucleotide sequence has at least 95% homology to SEQ ID NOS:3.

6. The genetically modified plant of claim 1, wherein the antisense exogenous FT-encoding nucleotide sequence comprises SEQ ID No:3.

7. The genetically modified plant of claim 1, further comprising a dominant negative mutation in a nucleotide sequence encoding a polypeptide selected from the group consisting of LEAFY (LFY), APETALA1 (AP1), CONSTANS (CO), FLORICAULA (FLO), SQUAMOSA (SQUA), FLOWERING LOCUS CA (FCA) and combinations thereof.

8. The genetically modified plant of claim 1, wherein the structural gene is operably associated with a regulatory nucleotide sequence.

9. The genetically modified plant of claim 8, wherein the regulatory nucleotide sequence is a promoter.

10. The genetically modified plant of claim 9, wherein the promoter is a constitutive promoter.

11. The genetically modified plant of claim 9, wherein the promoter is an inducible promoter.

12. The genetically plant of claim 1, wherein the nucleic acid further comprises a selectable marker.

13. The genetically plant of claim 1, wherein the plant is a dicotyledonous plant.

14. The genetically plant of claim 1, wherein the plant is a monocotyledonous plant.
15. A plant cell derived from the plant of claim 1.
16. Plant tissue derived from the plant of claim 1.
17. A seed which germinates into a plant comprising at least one exogenous antisense FT-encoding nucleotide sequence in its genome and having the phenotype of delayed flower development.
18. The seed of claim 17, wherein the least one exogenous antisense FT-encoding nucleotide sequence has at least 80% sequence homology to SEQ ID NO:3.
19. A vector containing a nucleotide sequence comprising at least one antisense FT sequence that inhibits flower development, operably associated with a promoter.
20. The vector of claim 19, wherein the at least one antisense FT sequence has at least 80% sequence homology to SEQ ID NO:3.
21. The vector of claim 19, wherein the vector comprises a T-DNA derived vector.
22. The vector of claim 19, further comprising an exogenous gene encoding a dominant negative mutation containing polypeptide selected from the group consisting of LEAFY (LFY), APETALA1 (AP1), CONSTANS (CO), FLORICAULA (FLO), SQUAMOSA (SQUA), FLOWERING LOCUS CA (FCA) and combinations thereof.
23. The vector of claim 19, wherein the promoter is a constitutive promoter.
24. The vector of claim 19, wherein the promoter is an inducible promoter.
25. A method for genetically modifying a plant cell such that a plant, produced from said cell, is characterized as having delayed flower development as compared with a wild-type plant, said method comprising:
- introducing at least one exogenous dominant negative mutation containing an FT encoding nucleotide sequence having at least 80% sequence homology to SEQ ID NO:1 into a plant cell in sense orientation to obtain a transformed plant cell; and
- growing the transformed plant cell under conditions which permit expression of a dominant negative mutation containing FT polypeptide encoded by the FT encoding nucleotide sequence, thereby producing a plant having inhibited flower development.
26. The method of claim 25, wherein said inhibited flower development is achieved by inhibiting expression or activity of an endogenous FT nucleotide sequence in the plant.

27. The method of claim 25, wherein said inhibited flower development is achieved by inducing expression of the dominant negative mutation containing FT polypeptide in the plant.

28. The method of claim 25, wherein said inhibited flower development is achieved by inducing expression of an antisense FT nucleotide sequence in the plant.

29. The method of claim 28, wherein said antisense FT nucleotide sequence comprises has at least 85% homology to SEQ ID NO: 3.

30. A genetically modified plant comprising a disrupted flowering time gene (*FT*), chromosomally integrated into the genome of the plant.

31. A method of producing a genetically modified plant comprising:

contacting a plant cell with a vector comprising a nucleotide sequence comprising at least a structural gene disrupting or interfering with expression of a flowering time gene encoded polypeptide to obtain a transformed plant cell;

producing a plant from said transformed plant cells; and

selecting a plant exhibiting late flower development relative to a wildtype plant.

32. The method of claim 31, wherein the structural gene is a dominant negative mutation in a nucleotide sequence encoding a polypeptide selected from the group consisting of FLOWERING LOCUS (T), LEAFY (LFY), APETALA1 (AP1), CONSTANS (CO), FLORICAULA (FLO), SQUAMOSA (SQUA), FLOWERING LOCUS CA (FCA) and combinations thereof..

33. The method of claim 31, wherein the structural gene is in an antisense orientation.

34. The method of claim 31, wherein the structural gene has at least 80% sequence homology to SEQ ID NO:3.

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